

Rec'd PCT/PTO 21 FEB 2006

**10/528423**

**RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,423  
Source: PCT  
Date Processed by STIC: 2/21/06

***ENTERED***



PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/538,423**

**DATE: 02/21/2006**  
**TIME: 12:55:10**

**Input Set : A:\PTO.KD.txt**  
**Output Set: N:\CRF4\02212006\J538423.raw**

3 <110> APPLICANT: Majumder, Arunendra  
 4 Manoj, Majee  
 6 <120> TITLE OF INVENTION: A salt tolerant L-myo-inositol 1-phosphate synthase and the  
 process of  
 7 obtaining the same  
 9 <130> FILE REFERENCE: 4544-051674  
 11 <140> CURRENT APPLICATION NUMBER: US 10/538,423  
 12 <141> CURRENT FILING DATE: 2005-06-10  
 14 <150> PRIOR APPLICATION NUMBER: PCT/IN2003/000065  
 15 <151> PRIOR FILING DATE: 2003-03-21  
 17 <160> NUMBER OF SEQ ID NOS: 3  
 19 <170> SOFTWARE: MicrosoftWord 2003  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1536  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Porteresia coarctata  
 26 <220> FEATURE:  
 28 <400> SEQUENCE: 1  
 29 atgttcatcg agagctccg cgtggagagc ccgcgcgtgc ggtacggcgc ggcggagatc 60  
 31 gagtcggagt accggtaacga cactacggag ctggtcacg agagccacga cggccgcctcg 120  
 33 cgctgggtcg tccgccccaa gtccgtccag taccacttca gacccagcac caccgtcccc 180  
 35 aagctcgaaa tcattgtcgat ggggtggggc ggcaacaacg gctcaacgct gacggctggg 240  
 37 gtcatcgcca gcaggaggaa aatctcatgg gcgaccaagg acaagggtgca gcaagccaaac 300  
 39 tactatggct cactcaccca ggcgtccacc atcaggtagt gaagctacaa cggggaggag 360  
 41 atctacgcgc ctttcaagag cttcctgccc atggtaacc ctgtatgacct tgtttcgaa 420  
 43 ggctgggaca tttagcaacat gaacctggct gatgttatga ccaggccaa ggtgctggac 480  
 45 attgatctgc agaagcagct taggccttac atggagtcct ggtgccttc cctggcatct 540  
 47 atgatcccgaa cttcatcgcc gctaaccagg gatccgcgc gaacaatgtc atcaaggaa 600  
 49 ccaagaagga gcagatgggg cagatcatca aaggacatca gggagttcaa ggaaaataac 660  
 51 aaaatggaca aggccgtgg ttttgtggact gcaaacactg aaaggtaaaa caattgtctg 720  
 53 tggttggct taatgaccaa tggaaaaacct tctgcgtctg tggacaggaa ccaggcggag 780  
 55 atatcgccat cgacatgttta ttgcattgc cttgcattcat tggagggtgt ccgtcaata 840  
 57 acgggagccc ttaaaaaaaaa atcttggccat ggaattgacg atcttggccat taaaaaaaaa 900  
 58 ctgcctgatc cggggggatt aattcaaaaaa agggcääac caaaaaaaaaa aaccggcttg 960  
 60 gttgatttcc tcatgggtgc tggaaaaaaag cccacccaa ttgtcagtttta caaccacttg 1020  
 62 gggaaataatg atggcacgaa ctttctcgcc cgcacacat tccgatccaa ggagatctcc 1080  
 64 aaaagcagcg tggtcgtatca catggcttcac agcaatgttca tcctctacga gcctggcgag 1140  
 66 catcctgatc atgttgcgt gattaagtat gtgcgtacg tcggagacag caagaggccc 1200  
 68 atggatgagt acacccatcaga gatcttcatg ggggttacaa acaccatcg tgcgcacaaac 1260  
 70 acctgcgagg actcgcttgc tggcgtacca atcatttttgc acctgggtgt cctggccgag 1320  
 72 ctcagcacta ggattcagct gaaaggcgag ggagaggaga aattccatcc ttccatccca 1380  
 74 gtggctacca tcctgatc ctcaccaag ggcgccttg ttccctctgg cacaccatcg 1440  
 76 gtggatcggcc tggcgtacca ggggtatcg ttcgatggc ttcgatggc 1500  
 78 ctggcccttg agaacaacat gatccctggag tacaag 1536

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80 <210> SEQ ID NO: 2  
 81 <211> LENGTH: 510  
 82 <212> TYPE: PRT  
 83 <213> ORGANISM: Oryza sativa  
 85 <220> FEATURE:  
 87 <400> SEQUENCE: 2.  
 89 Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly  
 90 1 5 10 15  
 92 Ala Ala Glu Ile Glu Ser Asp Tyr Gln Tyr Asp Thr Thr Glu Leu Val  
 93 20 25 30  
 95 His Glu Ser His Asp Gly Ala Ser Arg Tyr Ile Val Arg Pro Lys Ser  
 96 35 40 45  
 98 Val Arg Tyr Asn Phe Arg Thr Thr Thr Val Pro Lys Leu Gly Val  
 99 50 55 60  
 101 Met Leu Val Gly Tyr Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly  
 102 65 70 75 80  
 104 Val Ile Ala Asp Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val  
 105 85 90 95  
 107 Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg  
 108 100 105 110  
 110 Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu  
 111 115 120 125  
 113 Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile  
 114 130 135 140  
 115 Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp  
 116 145 150 155 160  
 118 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro  
 119 165 170 175  
 121 Leu Pro Gly Ile Tyr Asp Pro Asp Val Ile Ala Ala Asn Gln Gly Ser  
 122 180 185 190  
 124 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln  
 125 195 200 205  
 127 Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys  
 128 210 215 220  
 130 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys  
 131 225 230 235 240  
 133 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys  
 134 245 250 255  
 136 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val  
 137 260 265 270  
 139 Met Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val  
 140 275 280 285  
 142 Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly  
 143 290 295 300  
 145 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp  
 146 305 310 315 320  
 148 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn  
 149 325 330 335  
 151 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe

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**Output Set: N:\CRF4\02212006\J538423.raw**

152	340	345	350
154	Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser		
155	355	360	365
157	Ser Asn Ala Ile Leu Tyr Glu Leu Gly Glu His Pro Asp His Val Val		
158	370	375	380
160	Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp		
161	385	390	395
163	400		
164	Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu		
166	405	410	415
166	His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp		
167	420	425	430
169	Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu		
170	435	440	445
172	Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser		
173	450	455	460
175	Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn		
176	465	470	475
178	480		
179	Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys		
181	485	490	495
182	Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys		
184	500	505	510
184	<210> SEQ ID NO: 3		
185	<211> LENGTH: 512		
186	<212> TYPE: PRT		
187	<213> ORGANISM: Porteresia coarctata		
189	<220> FEATURE:		
191	<400> SEQUENCE: 3		
193	Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly		
194	5	10	15
196	Ala Ala Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val		
197	20	25	30
199	His Glu Ser His Asp Gly Ala Ser Arg Tyr Val Val Arg Pro Lys Ser		
200	35	40	45
202	Val Gln Tyr His Phe Arg Thr Ser Thr Thr Val Pro Lys Leu Gly Val		
203	50	55	60
205	Met Leu Val Gly Tyr Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly		
206	65	70	75
208	80		
209	Val Ile Ala Ser Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val		
211	85	90	95
211	Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg		
212	100	105	110
214	Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu		
215	115	120	125
217	Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile		
218	130	135	140
220	Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp		
221	145	150	155
223	160		
224	Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Trp Cys Leu		
	165	170	175

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226	Ser	Leu	Ala	Ser	Met	Ile	Pro	Thr	Ser	Ser	Pro	Leu	Thr	Arg	Asp	Pro
227				180				185				190				
229	Ala	Arg	Thr	Met	Ser	Ser	Arg	Glu	Pro	Arg	Arg	Ser	Arg	Trp	Gly	Arg
230				195				200				205				
232	Ser	Ser	Lys	Asp	Ile	Arg	Glu	Phe	Lys	Glu	Asn	Asn	Lys	Met	Asp	Lys
233				210				215				220				
235	Ala	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Asn	Asn	Cys	Leu
236	225				230				235				240			
238	Cys	Leu	Gly	Leu	Met	Thr	Asn	Gly	Lys	Pro	Ser	Ala	Ser	Val	Asp	Arg
239					245				250				255			
241	Asn	Gln	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Cys	His	Cys	Leu	Ala
242					260				265				270			
244	Ser	Leu	Glu	Gly	Val	Arg	Ser	Ile	Thr	Gly	Ala	Leu	Lys	Lys	Ser	
245					275				280				285			
247	Trp	Pro	Gly	Ile	Asp	Asp	Leu	Ala	Ile	Lys	Lys	Lys	Leu	Pro	Asp	Pro
248					290				295				300			
250	Gly	Gly	Leu	Ile	Gln	Lys	Arg	Gly	Lys	Pro	Lys	Lys	Lys	Thr	Gly	Leu
251	305					310				315				320		
253	Val	Asp	Phe	Leu	Met	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser
254						325				330				335		
256	Tyr	Asn	His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln
257						340				345				350		
259	Thr	Phe	Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Ser	Val	Val	Asp	Asp	Met
260						355				360				365		
262	Val	Ser	Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Leu	Gly	Glu	His	Pro	Asp	His
263						370				375				380		
265	Val	Val	Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala
266	385					390				395				400		
268	Met	Asp	Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Asn	Thr	Ile
269						405				410				415		
271	Val	Leu	His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile
272						420				425				430		
274	Leu	Asp	Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Gln	Leu	Lys
275						435				440				445		
277	Gly	Glu	Gly	Glu	Glu	Lys	Phe	His	Ser	Phe	His	Pro	Val	Ala	Thr	Ile
278						450				455				460		
280	Leu	Ser	Tyr	Leu	Thr	Lys	Ala	Pro	Leu	Val	Pro	Pro	Gly	Thr	Pro	Val
281	465					465				470				475		
283	Val	Asn	Ala	Leu	Ala	Lys	Gln	Arg	Ala	Met	Leu	Glu	Asn	Ile	Met	Arg
284						485				490				495		
287	Ala	Cys	Val	Gly	Leu	Ala	Pro	Glu	Asn	Asn	Met	Ile	Leu	Glu	Tyr	Lys
288						500				505				510		

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/538,423

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TIME: 12:55:11

Input Set : A:\PTO.KD.txt  
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